

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: June 9, 2005, 15:42:38 ; Search time 485 Seconds
(without alignments)
276.950 Million cell updates/sec

Title: US-09-856-114A-20
Perfect score: 604
Sequence: 1 QVQLVQSGAEVKGASVKV.....CAREYDEAYWGQGLTVTVSS 115

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA Main:*

- 1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US080_COMB.pep.*
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- 22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep.*
- 23: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
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- 25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep.*
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- 28: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
- 29: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*
- 30: /cgn2_6/ptodata/1/paa/US104_COMB.pep.*
- 31: /cgn2_6/ptodata/1/paa/US105_COMB.pep.*
- 32: /cgn2_6/ptodata/1/paa/US106_COMB.pep.*
- 33: /cgn2_6/ptodata/1/paa/US107_COMB.pep.*
- 34: /cgn2_6/ptodata/1/paa/US108_COMB.pep.*
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- 36: /cgn2_6/ptodata/1/paa/US110_COMB.pep.*
- 37: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	604	100.0	115	18	US-09-485-071A-20
2	604	100.0	115	23	US-09-856-114-20
3	604	100.0	115	23	US-09-856-114-20
4	572	94.7	115	18	US-09-485-071A-21
5	572	94.7	115	23	US-09-856-114-21
6	572	94.7	115	23	US-09-856-114-21
7	554	91.7	115	18	US-09-485-071A-33
8	537	88.9	115	18	US-09-485-071A-19
9	537	88.9	115	23	US-09-856-114-19
10	537	88.9	115	23	US-09-856-114A-19
11	517	85.6	119	35	US-10-981-738-30
12	509	84.3	119	35	US-10-981-738-32
13	508	84.1	119	35	US-10-981-738-36
14	508	84.1	119	35	US-10-981-738-46
15	506	83.8	119	35	US-10-981-738-34
16	505	83.6	119	35	US-10-981-738-40
17	505	83.6	119	35	US-10-981-738-44
18	504	83.4	119	35	US-10-981-738-38
19	503.5	83.4	119	22	US-09-791-537-126855
20	503	83.3	119	35	US-10-981-738-54
21	502	83.1	119	35	US-10-981-738-48
22	500	82.8	119	35	US-10-981-738-42
23	495	82.0	117	22	US-09-791-537-56245
24	492.5	81.5	161	22	US-09-791-537-6790
25	492	81.5	121	13	US-08-913-555-19
26	488.5	80.9	131	22	US-09-791-537-124399
27	488.5	80.9	139	17	US-09-367-833B-7
28	488.5	80.9	139	17	US-09-367-833B-8
29	488.5	80.9	139	19	US-09-509-098-50
30	488.5	80.9	139	19	US-09-509-098-127
31	488.5	80.9	139	19	US-09-509-530B-7
32	488.5	80.9	139	19	US-09-509-530B-8
33	488.5	80.9	139	20	US-09-622-646-28
34	488.5	80.9	139	22	US-09-622-646-29
35	488.5	80.9	139	22	US-09-760-723-7
36	488.5	80.9	139	22	US-09-760-723-8
37	488.5	80.9	139	28	US-10-218-253-125
38	488.5	80.9	139	28	US-10-218-253-128
39	488.5	80.9	139	29	US-10-315-125-7
40	488.5	80.9	139	29	US-10-315-125-8
41	488.5	80.9	139	30	US-10-428-085-7
42	488.5	80.9	139	30	US-10-428-085-8
43	488.5	80.9	139	30	US-10-474-714-6
44	488	80.8	119	28	US-10-233-996-4
45	488	80.8	123	23	US-09-842-776A-60

ALIGNMENTS

RESULT 1

US-09-485-071A-20
Sequence 20, Application US/09485071A
GENERAL INFORMATION:
APPLICANT: Hyo Jeong Hong
APPLICANT: Chun Jeih Ryu
APPLICANT: Hangsook Hur
TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR SURFACE
FILE REFERENCE: 118.13USWO
CURRENT APPLICATION NUMBER: US/09/485.071A
CURRENT FILING DATE: 2002-11-07
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 1998-49663
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20

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OM protein - protein search, using sw model

Run on: June 9, 2005, 15:45:18 ; Search time 57 Seconds
(without alignments)
242.260 Million cell updates/sec

Title: US-09-856-114A-20
Perfect score: 604
Sequence: 1 QVQLVQSGAEVVRFGASVKV'.....CAREYDAYWGQGLTVTVSS 115

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 561007 seqs, 120076725 residues

Total number of hits satisfying chosen parameters: 561007

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:*

- 1: /cgm2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgm2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgm2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgm2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgm2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgm2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgm2_6/ptodata/1/paa/US11_NEW_COMB.pep.*
- 8: /cgm2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	488.5	80.9	121	6	US-10-522-086-2
2	488.5	80.9	352	1	PCT-US05-06441-5
3	487	80.6	247	7	US-11-084-717-21
4	484.5	80.2	120	1	PCT-US04-37430-59
5	484.5	80.2	120	1	PCT-US04-37430-67
6	484	80.1	543	6	US-10-495-664-3
7	482	79.8	121	1	PCT-US04-29527-42
8	482	79.8	121	6	US-10-938-992-42
9	480.5	79.6	271	7	US-11-088-569-12
10	480.5	79.6	271	7	US-11-088-570-12
11	480.5	79.6	271	7	US-11-088-693-12
12	480.5	79.6	271	7	US-11-089-367-12
13	480.5	79.6	271	7	US-11-089-368-12
14	480.5	79.6	271	7	US-11-088-737-12
15	480.5	79.6	271	7	US-11-089-190-12
16	480.5	79.6	271	7	US-11-089-511-12
17	479	79.3	291	7	US-11-093-103-102
18	479	79.3	322	7	US-11-093-103-96
19	479	79.3	729	7	US-11-093-103-94
20	478	79.1	121	6	US-10-502-145-21
21	475	78.6	247	7	US-11-084-717-23
22	475	78.6	247	7	US-11-084-717-25
23	474.5	78.6	121	6	US-10-522-086-4
24	473	78.3	121	1	PCT-US04-37430-7
25	473	78.3	121	6	US-10-842-011A-7

26	471.5	78.1	122	6	US-10-412-703B-13
27	471.5	78.1	277	7	US-11-126-817-54
28	468	77.5	129	6	US-10-965-616-77
29	467.5	77.4	121	7	US-11-061-956-12
30	467.5	77.4	352	1	PCT-US05-06441-6
31	467	77.3	117	5	US-09-490-084-22
32	466	77.2	447	1	PCT-US05-11996-130
33	466	77.2	447	1	PCT-US05-11996-131
34	466	77.2	447	1	PCT-US05-11996-132
35	466	77.2	447	1	PCT-US05-11996-133
36	466	77.2	447	1	PCT-US05-11996-134
37	466	77.2	447	7	US-11-102-621-130
38	466	77.2	447	7	US-11-102-621-131
39	466	77.2	447	7	US-11-102-621-132
40	466	77.2	447	7	US-11-102-621-133
41	466	77.2	447	7	US-11-102-621-134
42	465.5	77.1	277	7	US-11-126-817-52
43	465	77.0	119	7	US-11-089-331-79
44	464.5	76.9	116	7	US-11-021-819A-10
45	464.5	76.9	122	1	PCT-US04-41788-29

ALIGNMENTS

RESULT 1
US-10-522-086-2
; Sequence 2, Application US/10522086
; GENERAL INFORMATION:
; APPLICANT: Koga, Takaki
; APPLICANT: Suzuki, Tsukasa
; APPLICANT: Saito, Hiroyuki
; TITLE OF INVENTION: NON-NEUTRALIZING ANTI-APC ANTIBODIES
; FILE REFERENCE: 14875-138U1
; CURRENT APPLICATION NUMBER: US/10/522,086
; CURRENT FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: PCT/JP2003/009087
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: JP 2002-212582
; PRIOR FILING DATE: 2002-07-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-522-086-2

Query Match	80.9%	Score 488.5	DB 6	Length 121
Best Local Similarity	79.2%	Pred. No. 2.4e-27		
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Qy	1	QVQLVQSGAEVVRFGASVKYCKASGYAFSSSWNNVROAPQGLGWIGRIYPGDNTY	60	
Db	1	QVQLQQSGPELVKPGASVKISCKASGYAFSSSWNNVQKQPGGLEWIGRIYPGDNTY	60	
Qy	61	AQKFGKATITADKSTSTAYMELSSLSSEPTAVYFCAR-----EYDAYWGQGLTVTVSS	115	
Db	61	NGKFRGKATITADKSSSTATYQLTSLTSDVSAVYFCARWGITTAAWPAWVGQGLTVTVSA	120	

RESULT 2
PCT-US05-06441-5
; Sequence 5, Application PC/TUS0506441
; GENERAL INFORMATION:
; APPLICANT: University of Tennessee Research Foundation
; APPLICANT: Radiac, Marko
; TITLE OF INVENTION: METHODS OF IDENTIFYING APOPTOTIC CELLS
; FILE REFERENCE: 1306/23 PCT
; CURRENT APPLICATION NUMBER: PCT/US05/06441
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/556,279
; PRIOR FILING DATE: 2004-04-29

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OM protein - protein search, using sw model

Run on: June 9, 2005, 15:48:14 ; Search time 154 Seconds
(without alignments)
286.256 Million cell updates/sec

Title: US-09-856-114A-20
Perfect score: 604
Sequence: 1 QVQLVQSGAEVVKPGASVKV.....CARRYDEAYWGQGLTVTVSS 115

Scoring table: BLASUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	488.5	80.9	139	9 US-09-760-723-7	Sequence 7, Appli
2	488.5	80.9	139	9 US-09-760-723-8	Sequence 8, Appli
3	488.5	80.9	139	9 US-09-355-925-7	Sequence 7, Appli
4	488.5	80.9	139	9 US-09-355-925-8	Sequence 8, Appli
5	488.5	80.9	139	10 US-09-269-921-125	Sequence 125, App
6	488.5	80.9	139	10 US-09-269-921-128	Sequence 128, App
7	488.5	80.9	139	10 US-09-509-098-50	Sequence 50, Appl
8	488.5	80.9	139	10 US-09-509-098-127	Sequence 127, App
9	488.5	80.9	139	14 US-10-315-125-7	Sequence 7, Appli
10	488.5	80.9	139	14 US-10-315-125-8	Sequence 8, Appli
11	488.5	80.9	139	14 US-10-218-253-125	Sequence 125, App

12	488.5	80.9	139	14	US-10-218-253-128	Sequence 128, App
13	488.5	80.9	139	14	US-10-428-085-7	Sequence 7, Appli
14	488.5	80.9	139	14	US-10-428-085-8	Sequence 8, Appli
15	488.5	80.9	139	16	US-10-474-714-6	Sequence 6, Appli
16	488.5	80.8	139	14	US-10-233-996-4	Sequence 4, Appli
17	488.5	80.8	139	14	US-09-842-776A-60	Sequence 60, Appl
18	487.5	80.7	139	10	US-09-269-921-111	Sequence 111, App
19	487.5	80.7	139	10	US-09-269-921-117	Sequence 117, App
20	487.5	80.7	139	10	US-09-509-098-22	Sequence 22, Appl
21	487.5	80.7	139	10	US-09-509-098-34	Sequence 34, Appl
22	487.5	80.7	139	14	US-10-218-253-111	Sequence 111, App
23	487.5	80.7	139	14	US-10-218-253-117	Sequence 117, App
24	487.5	80.6	247	15	US-10-620-278-21	Sequence 21, Appl
25	487.5	80.6	247	17	US-10-620-049-21	Sequence 21, Appl
26	484.5	80.2	139	10	US-09-269-921-110	Sequence 110, App
27	484.5	80.2	139	10	US-09-269-921-112	Sequence 112, App
28	484.5	80.2	139	10	US-09-269-921-113	Sequence 113, App
29	484.5	80.2	139	10	US-09-509-098-20	Sequence 20, Appl
30	484.5	80.2	139	10	US-09-509-098-24	Sequence 24, Appl
31	484.5	80.2	139	10	US-09-509-098-26	Sequence 26, Appl
32	484.5	80.2	139	14	US-10-218-253-110	Sequence 110, App
33	484.5	80.2	139	14	US-10-218-253-112	Sequence 112, App
34	484.5	80.2	139	14	US-10-218-253-113	Sequence 113, App
35	483.5	80.0	119	14	US-10-233-996-2	Sequence 2, Appli
36	482.5	79.9	139	10	US-09-269-921-123	Sequence 123, App
37	482.5	79.9	139	10	US-09-509-098-46	Sequence 46, Appl
38	482.5	79.9	139	14	US-10-218-253-123	Sequence 123, App
39	481.5	79.7	124	17	US-10-903-858-10	Sequence 10, Appl
40	481.5	79.7	124	17	US-10-903-858-15	Sequence 15, Appl
41	481.5	79.7	139	10	US-09-269-921-109	Sequence 109, App
42	481.5	79.7	139	10	US-09-269-921-115	Sequence 115, App
43	481.5	79.7	139	10	US-09-509-098-18	Sequence 18, Appl
44	481.5	79.7	139	10	US-09-509-098-30	Sequence 30, Appl
45	481.5	79.7	139	14	US-10-218-253-109	Sequence 109, App

ALIGNMENTS

RESULT 1
US-09-760-723-7
; Sequence 7, Application US/09760723
; Patent No. US20020034507A1
; GENERAL INFORMATION:
; APPLICANT: KOISHIHARA, YASUO
; TITLE OF INVENTION: INHIBITOR OF LYMPHOCYTE ACTIVATION
; FILE REFERENCE: 053466/0295
; CURRENT APPLICATION NUMBER: US/09/760,723
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/367,833
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: PCT/JP98/00831
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 7
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of H chain V region version r of humanized
; OTHER INFORMATION: anti-HM1.24 antibody
US-09-760-723-7

Query Match 80.9%; Score 488.5; DB 9; Length 139;
Best Local Similarity 78.3%; Pred. No. 26-35;
Matches 94; Conservative 8; Mismatches 13; Indels 5; Gaps 1;
QY 1 QVQLVQSGAEVVKPGASVKASGYSFSSSWMMVTRQAPCGGLEWIGRIYVPGDITNY 60
DB 20 QVQLVQSGAEVVKPGASVKASGYSFTTPYVQMWVRQAPCGGLEWMSIFPGDITRY 79

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 9, 2005, 15:36:45 ; Search time 42 Seconds
(without alignments)
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Title: US-09-856-114A-20
Perfect score: 604
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /cgm2_6/ptodata/1/1aa/5A_COMB.pep.*
- 2: /cgm2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgm2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgm2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgm2_6/ptodata/1/1aa/6C_COMB.pep.*
- 6: /cgm2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	488.5	80.9	139	4	US-09-355-925-7
2	488.5	80.9	139	4	US-09-355-925-8
3	488.5	80.9	139	4	US-09-269-921-125
4	488.5	80.9	139	4	US-09-269-921-128
5	488	80.8	119	4	US-09-438-954-4
6	487.5	80.7	139	4	US-09-269-921-111
7	487.5	80.7	139	4	US-09-269-921-117
8	484.5	80.2	139	4	US-09-269-921-110
9	484.5	80.2	139	4	US-09-269-921-112
10	484.5	80.2	139	4	US-09-269-921-113
11	483	80.0	119	4	US-09-438-954-2
12	482.5	79.9	139	4	US-09-269-921-123
13	482	79.8	120	3	US-09-065-059-1
14	481.5	79.7	139	4	US-09-269-921-109
15	481.5	79.7	139	4	US-09-269-921-115
16	478.5	79.2	139	4	US-09-269-921-108
17	478.5	79.2	139	4	US-09-269-921-118
18	477.5	79.1	139	4	US-09-269-921-122
19	477.5	79.1	249	2	US-08-797-689-18
20	477.5	79.1	249	4	US-09-984-186-18
21	475.5	78.7	139	4	US-09-269-921-121
22	475	78.6	119	4	US-09-254-180C-18
23	474.5	78.6	139	4	US-09-269-921-124
24	473.5	78.4	139	4	US-09-269-921-114
25	472.5	78.2	118	3	US-08-513-968-80
26	472.5	78.2	139	4	US-09-269-921-119
27	472	78.1	119	4	US-09-254-180C-19

28	469.5	77.7	139	4	US-09-269-921-116	Sequence 116, Appl
29	469	77.6	119	1	US-08-458-516-10	Sequence 10, Appl
30	469	77.6	121	1	US-07-634-278-53	Sequence 53, Appl
31	469	77.6	121	1	US-08-477-728-53	Sequence 53, Appl
32	469	77.6	121	1	US-08-474-040-53	Sequence 53, Appl
33	469	77.6	121	1	US-08-487-200-53	Sequence 53, Appl
34	469	77.6	121	3	US-08-484-537-53	Sequence 45, Appl
35	469	77.6	222	1	US-08-458-516-22	Sequence 22, Appl
36	469	77.6	235	1	US-08-458-516-23	Sequence 23, Appl
37	469	77.6	449	1	US-08-458-516-13	Sequence 13, Appl
38	468.5	77.6	139	4	US-09-269-921-120	Sequence 120, Appl
39	468	77.5	129	2	US-08-561-521-45	Sequence 45, Appl
40	468	77.5	129	3	US-08-525-539A-77	Sequence 77, Appl
41	468	77.5	129	5	PCT-US95-01219-45	Sequence 45, Appl
42	467	77.3	117	3	US-09-025-769B-22	Sequence 22, Appl
43	467	77.3	117	4	US-09-490-070A-22	Sequence 22, Appl
44	467	77.3	117	4	US-09-490-153-22	Sequence 22, Appl
45	467	77.3	117	4	US-09-490-324-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-09-355-925-7
; Sequence 7, Application US/09355925
; Patent No. 6503510
; GENERAL INFORMATION:
; APPLICANT: KOISHIHARA, YASUO
; APPLICANT: YOSHIMURA, YASUSHI
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
; FILE REFERENCE: 053466/0255
; CURRENT APPLICATION NUMBER: US/09/355.925
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/JP98/00568
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: JP 9-41410
; PRIOR FILING DATE: 1997-02-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of H chain V region version r of
; OTHER INFORMATION: humanized anti-HM1.24 antibody
US-09-355-925-7

Query Match 80.9%; Score 488.5; DB 4; Length 139;
Best Local Similarity 78.3%; Pred. No. 1.2e-39;
Matches 94; Conservative 8; Mismatches 13; Indels 5; Gaps 1;

Qy	1	QVQLVQSGAEVVKFGASVKVSKASGVAFSSNNWVQAPQGLEWIGRIYFGDITVY 60
Db	20	QVQLVQSGAEVVKFGASVKVSKASGVTFPTVMQVQAPQGLEWISIFPGDITRY 79
Qy	61	AKQFGKATLTADKSTSTAYMELSLRSEDYAVYFCAR-----EYDEAYWGQGLTVTVSS 115
Db	80	SQPKRGVMTADKSTSTAYMELSLRSEDYAVYFCARGLRGGYTFDYGQGLTVTVSS 139

RESULT 2

US-09-355-925-8
; Sequence 8, Application US/09355925
; Patent No. 6503510
; GENERAL INFORMATION:
; APPLICANT: KOISHIHARA, YASUO
; APPLICANT: YOSHIMURA, YASUSHI
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
; FILE REFERENCE: 053466/0255
; CURRENT APPLICATION NUMBER: US/09/355.925

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OM protein - protein search, using sw model

Run on: June 9, 2005, 15:13:32 ; Search time 174 Seconds
(without alignments)
338.443 Million cell updates/sec

Title: US-09-856-114A-20
Perfect score: 604
Sequence: 1 QVQLVQSGAEVKEPGASVKV.....CAREYDAYWQGTGLTVSS 115

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_spot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	512	84.8	614	2 Q7TWT6	Q7TWT6 mus musculus
2	459	76.0	464	2 Q6PF95	Q6PF95 mus musculus
3	457	75.7	473	2 Q9D8L4	Q9D8L4 mus musculus
4	456.5	75.6	118	2 Q921C4	Q921C4 mus musculus
5	456	75.5	474	2 Q8R3H6	Q8R3H6 mus musculus
6	452.5	74.9	124	2 Q9UL92	Q9UL92 homo sapien
7	451	74.7	111	2 Q9D9B8	Q9D9B8 mus musculus
8	441.5	73.1	110	2 Q9JL83	Q9JL83 mus musculus
9	440	72.8	142	2 Q924Q1	Q924Q1 mus musculus
10	439	72.7	140	2 Q924R2	Q924R2 mus musculus
11	435.5	72.1	143	2 Q924P9	Q924P9 mus musculus
12	435.5	72.1	143	2 Q924Q0	Q924Q0 mus musculus
13	435.5	72.1	145	2 Q924R4	Q924R4 mus musculus
14	435	72.0	140	2 Q924P8	Q924P8 mus musculus
15	434.5	71.9	159	2 Q96QSO	Q96QSO homo sapien
16	434	71.9	244	2 Q65ZC8	Q65ZC8 homo sapien
17	434	71.9	481	2 Q91WT1	Q91WT1 mus musculus
18	432.5	71.6	141	2 Q924Q4	Q924Q4 mus musculus
19	432.5	71.6	143	2 Q924R0	Q924R0 mus musculus
20	432.5	71.6	498	2 Q6N041	Q6N041 homo sapien
21	431.5	71.4	143	2 Q924Q5	Q924Q5 mus musculus
22	431.5	71.4	482	2 Q8K172	Q8K172 mus musculus
23	431	71.4	146	2 Q924Q3	Q924Q3 mus musculus
24	430.5	71.3	463	2 Q99LCA	Q99LCA mus musculus
25	430	71.2	119	2 Q9GY22	Q9GY22 schistosoma
26	429.5	71.1	139	2 Q924R5	Q924R5 mus musculus
27	429.5	71.1	145	2 Q924Q6	Q924Q6 mus musculus
28	429.5	71.1	145	2 Q924Q9	Q924Q9 mus musculus
29	429.5	71.1	145	2 Q924R1	Q924R1 mus musculus
30	429.5	71.1	613	2 Q8VCX7	Q8VCX7 mus musculus
31	429	71.0	146	2 Q924R8	Q924R8 mus musculus

32	428	70.9	119	2 Q9UL94	Q9UL94 homo sapien
33	426.5	70.6	518	2 Q6N030	Q6N030 homo sapien
34	426	70.5	142	2 Q924Q2	Q924Q2 mus musculus
35	425.5	70.4	136	2 Q7TPE3	Q7TPE3 mus musculus
36	425.5	70.4	137	2 Q924R6	Q924R6 mus musculus
37	424.5	70.3	139	1 HV07 MOUSE	P01751 mus musculus
38	424.5	70.3	145	2 Q924P7	Q924P7 mus musculus
39	424.5	70.3	145	2 Q924Q7	Q924Q7 mus musculus
40	423	70.0	146	2 Q924Q8	Q924Q8 mus musculus
41	421.5	69.8	143	2 Q91V67	Q91V67 mus musculus
42	421.5	69.8	465	2 Q6PJB2	Q6PJB2 mus musculus
43	421	69.7	125	2 Q9UL95	Q9UL95 homo sapien
44	421	69.7	134	2 Q65ZR6	Q65ZR6 mus musculus
45	418.5	69.3	116	2 Q9UL89	Q9UL89 homo sapien

ALIGNMENTS

RESULT 1

ID	Q7TWT6	PRELIMINARY;	PRT;	614 AA.
AC	Q7TWT6;			
DT	01-OCT-2003 (TrEMBLrel. 25, Created)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	MGC60843 protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CS7BL/6NCR; TISSUE=Hematopoietic Stem Cell;			
FX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Hopkins R.F., Jordan H., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Diatchenko L., Matsumura K., Casavant T.L., Scheetz T.E.,			
RA	Stapleton M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fabry J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[2]			
RC	SEQUENCE FROM N.A.			
RA	STRAIN=CS7BL/6NCR; TISSUE=Hematopoietic Stem Cell;			
RA	Strausberg R.;			
RL	Submitted (JUN-2003) to the ENBL/GenBank/DBJ databases.			
DR	EMBL; BC053409; AAHS3409.1; -			
DR	HSSP; P01820; 1G7J.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG CI.			
DR	InterPro; IPR003006; IG MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF07654; CI-set; 4.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS00835; IG LIKE; 5.			
DR	PROSITE; PS00290; IG MHC; UNKNOWN 3.			
SQ	SEQUENCE 614 AA; 67746 MW; 839BAF3B8D124F89 CRC64;			

Query Match 84.8%; Score 512; DB 2; Length 614;

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OM protein - protein search, using sw model

Run on: June 9, 2005, 15:15:17 ; Search time 39 Seconds
(without alignments)
283.716 Million cell updates/sec

Title: US-09-856-114A-20
Perfect score: 604
Sequence: 1 QVQLVQSGAEVVKPGASVKV.....CAREYDRAYWGQGLTVTVSS 115

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	503.5	83.4	119	2 A24672	Ig heavy chain pre
2	486	80.5	118	2 PL0231	Ig heavy chain v r
3	474.5	78.6	117	2 PL0237	Ig heavy chain v r
4	474	78.5	112	2 PL0232	Ig heavy chain v r
5	473.5	78.4	117	2 PL0235	Ig heavy chain v r
6	473.5	78.4	140	2 S09216	Ig heavy chain pre
7	471.5	78.1	115	2 PL0238	Ig heavy chain v r
8	465.5	77.1	116	2 S09962	Ig heavy chain v-D
9	463	76.7	109	2 PL0233	Ig heavy chain v r
10	462.5	76.6	118	2 S36265	Ig heavy chain v r
11	458.5	75.9	120	2 B22769	Ig heavy chain v r
12	456.5	75.6	117	2 PL0234	Ig heavy chain v r
13	453	75.0	119	2 D30562	Ig heavy chain v r
14	452	74.8	138	2 S21810	Ig heavy chain v r
15	451	74.7	142	2 A32483	Ig heavy chain v r
16	450	74.5	119	2 C30562	Ig heavy chain v r
17	448.5	74.3	135	2 S49530	anti-8m antibody v
18	448	74.2	119	2 E30562	Ig heavy chain v r
19	445	73.7	129	2 A33548	Ig heavy chain v-1
20	444.5	73.6	120	2 PH0962	Ig heavy chain v r
21	443.5	73.4	135	2 A30577	Ig heavy chain pre
22	443	73.3	138	2 E32513	Ig heavy chain pre
23	441	73.0	119	2 PH0961	Ig heavy chain v r
24	440.5	72.9	128	2 PH0952	Ig heavy chain v r
25	439.5	72.8	137	2 F29380	Ig heavy chain pre
26	439	72.7	123	2 D33548	Ig heavy chain v-1
27	438.5	72.6	120	2 S41394	Ig heavy chain v r
28	438.5	72.6	137	2 E29380	Ig heavy chain pre
29	438	72.5	121	2 S20783	Ig heavy chain v r

30	438	72.5	125	2 PH0957	Ig heavy chain v r
31	437.5	72.4	141	2 A39276	Ig heavy chain pre
32	436.5	72.3	116	2 PH0959	Ig heavy chain v r
33	436.5	72.3	116	2 S53751	antibody Fab Jel 1
34	434.5	71.9	120	2 PD0008	Ig heavy chain v r
35	434.5	71.9	122	2 S24287	Ig heavy chain v r
36	432.5	71.6	120	2 G28195	Ig heavy chain v r
37	432.5	71.6	136	2 PH0960	Ig heavy chain v r
38	431.5	71.4	120	2 F28195	Ig heavy chain v r
39	431.5	71.4	122	2 PH0958	Ig heavy chain v r
40	431	71.4	129	2 S46393	Ig heavy chain v r
41	429.5	71.1	132	2 PH0954	Ig heavy chain v r
42	429	71.0	119	2 PL0086	Ig heavy chain v r
43	428.5	70.9	118	2 C30560	Ig heavy chain v r
44	428.5	70.9	135	2 P50057	Ig heavy chain pre
45	428.5	70.9	141	2 JL0076	Ig heavy chain pre

ALIGNMENTS

RESULT 1

A24672

Ig heavy chain precursor V region (VMU-3.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999

C:Accession: A24672

R:Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A:Reference number: A91022; MUID:86055722; PMID:2998759

A:Accession: A24672

A:Molecule type: DNA

A:Residues: 1-119 <WIN>

A:Cross-references: GB:X03088; NID:G52378; PIDN:CAA26881.1; PID:G773578

A>Note: this sequence was determined from the germline gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:4-119/Product: Ig heavy chain V region VMU-3.2 #status predicted <MAT>

F:18-101/Domain: immunoglobulin homology <IMM>

Query Match 83.4%; Score 503.5; DB 2; Length 119;

Best Local Similarity 81.9%; Pred. No. 8.7e-39;

Matches 95; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVVKPGASVKISCKASGYAFSSSMWVWVQAPCGGLEWIGRIYFGDGTNY 60

Db 4 QVQLQSGPELVKPGASVKISCKASGYAFSSSMWVWVQAPCGGLEWIGRIYFGDGTNY 63

QY 61 AQKPGKATLTADKSTSTAYMELSLRSEDYAVYFCARE-YDEAYWGQGLTVTVSS 115

Db 64 NGKPKGKATLTADKSSSTAYMQLSLTSEDSAVYFCARDYGSIDYWGQGLTVTVSS 119

RESULT 2

PL0231

Ig heavy chain V region (anti-DNA, D20VH) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0231

R:Shlomchik, M.; Maccelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J.

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231; MUID:90111618; PMID:2104919

A:Accession: PL0231

A:Molecule type: mRNA

A:Residues: 1-118 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-49/Region: framework 2

F:50-66/Region: complementarity-determining 2

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OM protein - protein search, using sw model

Run on: June 9, 2005, 15:12:11 ; Search time 161 Seconds
(without alignments)
276.257 Million cell updates/sec

Title: US-09-856-114A-20
Perfect score: 604
Sequence: 1 QVQLVQSGAEVVKPGASVKY.....CAREYDRAYWCGQLTVTVSS 115

Scoring table: BLOSUM62

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	604	100.0	115	3 AAB12168	Aab12168 Humanised
2	588	97.4	115	7 ADE13224	Ade13224 Humanised
3	572	94.7	115	3 AAB12169	Aab12169 Humanised
4	554	91.7	115	3 AAB12172	Aab12172 Humanised
5	537	88.9	115	3 AAU76446	Aau76446 Mouse mon
6	537	88.9	115	3 AAB12167	Aab12167 Mouse HBV
7	537	88.9	115	7 ADE13216	Ade13216 Humanised
8	512	84.8	115	7 ADE13190	Ade13190 HZVII hea
9	492	81.5	121	8 AAU00833	Aau00833 Variable
10	488.5	80.9	121	8 ADJ25647	Adj25647 Mouse act
11	488.5	80.9	139	2 AAU65774	Aau65774 Anti-huma
12	488.5	80.9	139	2 AAU65773	Aau65773 Anti-huma
13	488.5	80.9	139	2 AAU62205	Aau62205 Humanised
14	488.5	80.9	139	2 AAU62206	Aau62206 Humanised
15	488.5	80.9	139	2 AAU02575	Aau02575 Humanised
16	488.5	80.9	139	2 AAU02572	Aau02572 Humanised
17	488.5	80.9	139	2 AAU32771	Aau32771 Anti-HM1
18	488.5	80.9	139	2 AAU32770	Aau32770 Anti-HM1
19	488.5	80.9	139	2 AAU05487	Aau05487 H chain V
20	488.5	80.9	139	2 AAU05486	Aau05486 H chain V
21	488.5	80.9	139	5 AAU52354	Aau52354 H chain V
22	488.5	80.9	139	5 AAU52355	Aau52355 H chain V
23	488.5	80.9	139	6 ABG71946	Abg71946 Human res
24	488.5	80.9	139	8 ADO60011	Ado60011 H chain V
25	488.5	80.9	139	8 ADO60010	Ado60010 H chain V

26	488.5	80.9	140	2 AAU77294	Aau77294 HM1.24 an
27	488	80.8	119	3 AAU71241	Aau71241 Humanised
28	488	80.8	123	3 AAB10024	Aab10024 H. pylori
29	488	80.8	123	4 AAB86074	Aab86074 H. pylori
30	487.5	80.7	139	2 AAU62212	Aau62212 Humanised
31	487.5	80.7	139	2 AAU02558	Aau02558 Humanised
32	487.5	80.7	139	2 AAU02564	Aau02564 Humanised
33	487	80.6	119	8 ADP84927	Adp84927 Variable
34	487	80.6	121	2 AAU10541	Aau10541 Chimeric
35	487	80.6	247	8 ADK42701	Adk42701 14B7 scFv
36	486	80.5	119	8 ADP84921	Adp84921 Variable
37	485	80.3	123	4 AAB86110	Aab86110 H. pylori
38	484.5	80.2	139	2 AAU62216	Aau62216 Humanised
39	484.5	80.2	139	2 AAU62211	Aau62211 Humanised
40	484.5	80.2	139	2 AAU62213	Aau62213 Humanised
41	484.5	80.2	139	2 AAU02557	Aau02557 Humanised
42	484.5	80.2	139	2 AAU02559	Aau02559 Humanised
43	484.5	80.2	139	2 AAU02560	Aau02560 Humanised
44	484	80.1	543	7 ADD12876	Add12876 CD28/mela
45	483	80.0	119	3 AAU71239	Aau71239 Humanised

ALIGNMENTS

RESULT 1

AAAB12168	Humanised HBV pre-S1 antibody HKR127HC (1) heavy chain variable region.
ID	AAAB12168 standard; protein; 115 AA.
XX	AAAB12168;
XX	AC
XX	12-SEP-2003 (revised)
DT	17-JAN-2001 (first entry)
DT	Humanised HBV pre-S1 antibody HKR127HC (1) heavy chain variable region.
XX	Humanised antibody; HBV surface antigen pre-S1; mouse; human;
XX	hepatitis B; liver cirrhosis; liver cancer.
OS	Homo sapiens.
OS	Mus sp.
OS	Chimeric.
XX	WO2000031141-A1.
PN	02-JUN-2000.
XX	02-JUN-2000.
PD	19-NOV-1999; 99WO-KR000699.
XX	19-NOV-1999; 98KR-00049663.
XX	(KOAD) KOREA ADV INST SCI & TECHNOLOGY.
PA	(GREG) KOREA GREEN CROSS CORP.
XX	Hong HJ, Ryu CJ, Hur H;
PI	WPI; 2000-400048/34.
XX	N-PSDB; AAAG2118.
DR	Humanized antibody specific for hepatitis B virus surface antigen pre-S1,
DR	containing humanized heavy and light chain regions, useful for preventing
XX	hepatitis B virus (HBV) infection and for treating chronic hepatitis B.
XX	Claim 2; Fig 1; 61pp; English.
XX	Hepatitis B virus (HBV) is responsible for hepatitis infection in humans,
CC	which may progress to liver cirrhosis or cancer. One of HBV's surface
CC	antigens is pre-S1. Monoclonal antibodies specific for pre-S1 antigen may
CC	efficiently neutralise HBV. The present invention relates to humanised
CC	antibodies specific for HBV surface antigen pre-S1. The humanised
CC	antibodies are useful for preventing HBV infection and for treating
CC	chronic hepatitis B. The Complementarity Determining Regions of mouse pre
CC	-S1 antibody HKR127 were grafted onto human antibody to produce the

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